

FIGURE 2

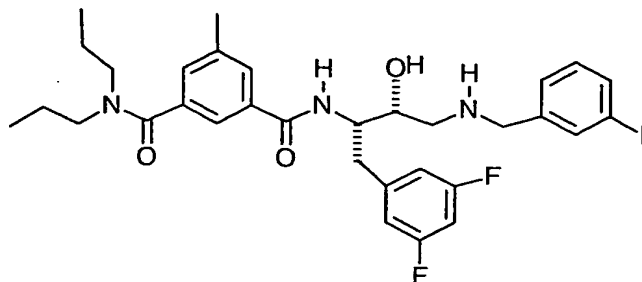


FIGURE 2

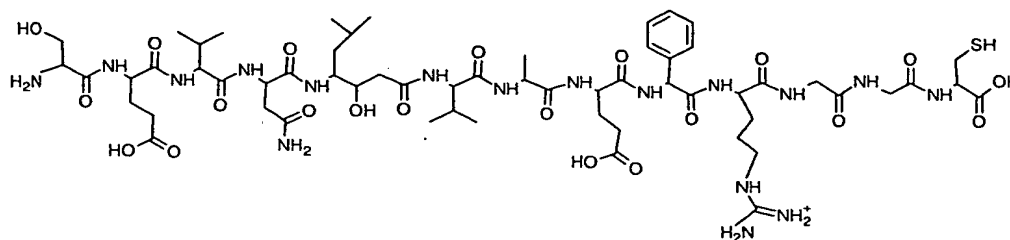


FIGURE 3

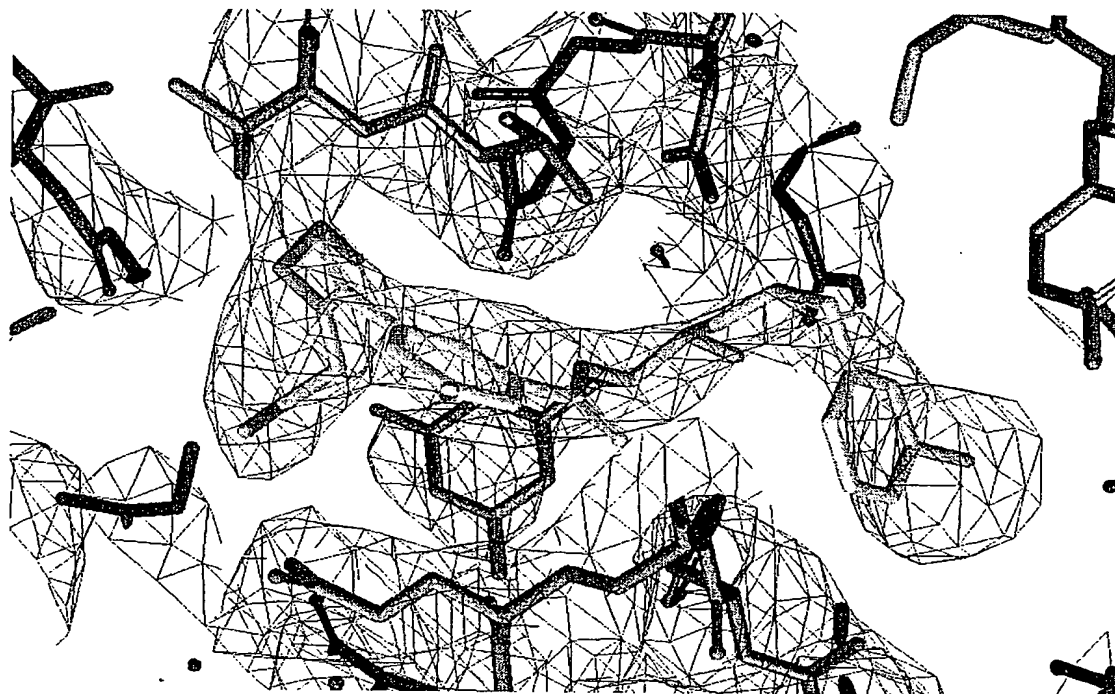


Figure 3 is a 3D molecular model of a glycosylated human beta-secretase enzyme. The protein backbone is shown as a wireframe mesh, and the attached carbohydrate chains are depicted as thick, dark, stick-like structures. The model is oriented with the active site region towards the bottom left. The glycan chains are complex, featuring various sugar residues and branching patterns. The overall structure is compact and globular, with the glycan chains extending from the protein surface.

FIGURE 4

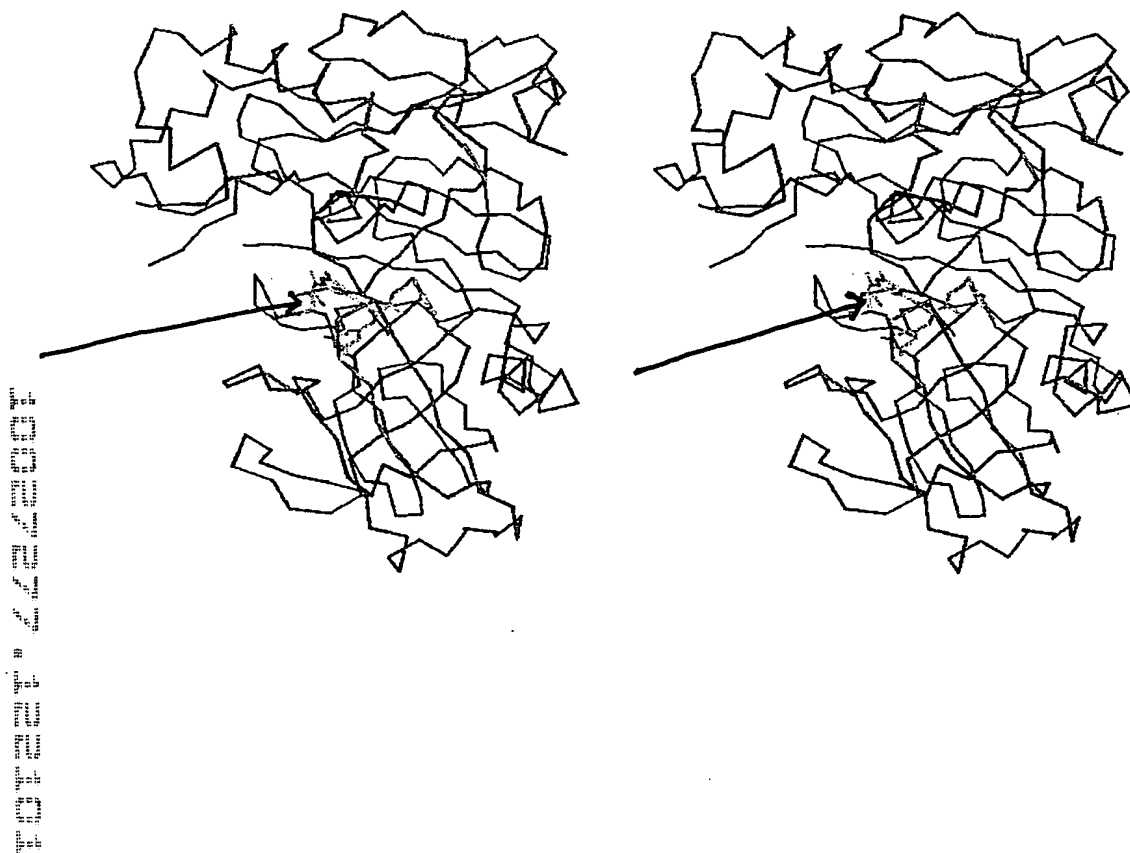


FIGURE 5



Figure 5 shows two views of the structure of the enzyme. The left view is a side view and the right view is a top view. The structure is a complex, three-dimensional representation of the enzyme's structure, showing the intricate folding of the polypeptide chain. The two models are identical, suggesting they represent different views or states of the same protein structure.

FIGURE 6

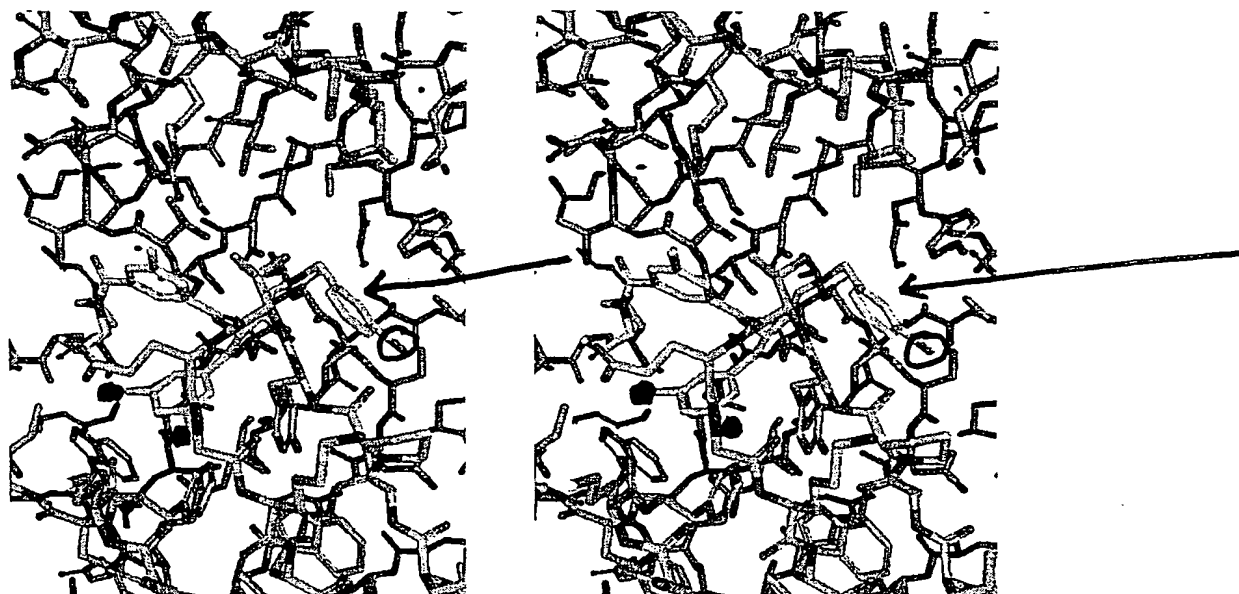


Figure 6 shows two molecular models of glycosylated human beta secretase. The models are rendered in a stick representation, showing the backbone and side chains of the protein, with various atoms represented by different symbols (e.g., circles, squares, triangles). The glycosylation is shown as branching structures extending from the protein backbone. A horizontal line with arrows at both ends connects the two models, indicating a comparison or transition between the two states.

FIGURE 7

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EMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFAVGAAPHPFLHRYQR
QLSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSN
WEGILGLAYAEIARPDDSLPFFDSLQKQTHVPNLFSLQCGAGFPLNQSEVLASVGGSM
IIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL
RLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ
SFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGF
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